





Qy 841 tctagqcaaaaagaaagctcagttgggttttcacgagtggttctgtgcttatattcagttct 900
Db 12841 TCTAGGC'AAAAGAAAAGCTCAGTTGGGTTTCACGAGTGTTCTGTGCTTATATTCAGTCT 12900

Qy 901 gtgectacatgtttctcatgcatgtctaacctgattttacctcttaacctgtaacctarettta 960
Db 12901 GTGCCTACATGTTCTCATGCAATGCTAACCCTGATTACCTCTTACCTGTAAAGCTACCTTA 12960

Qy 961 tcatgtggttttttaattgacagtcactcagccatttttaagcaaatatagtaagttcttt 1020
Db 12961 TCATGTGGCTTTTAATTGAC'AGTC'ACTCAGCCATTTC'AAAGCAGATAIAGTAGTACTTT 13020

Qy 1021 caqaactcacattgacaaatttataaaaagatgacttaaggtgaaagtgaagacaaaatcaca 1080
Db 13021 CAGAAGTCACATGGG'AAAGTGTAAAAAGATGACTTAAGGTGAAGTGAGGAC'AAAATCACA 13080

Qy 1081 ttctgcatactaacctatttttttctccctttaaggtgctaaacttgcacctcatctcca 1140
Db 13081 TTCTG'ATACTAACTATT'TTTTCTCCCTTTAAGGTGCTAAACTTGCACTCATGTGCA 13140

Qy 1141 ctcaatcaaaagtatttggagcgtagagcacaagcctcactcagctctgaaaggttaatacaq 1200
4/ 13141 CTCAGTAACAAGTATTGGGACGTAGAGCACAGCCTCACTCAGCTCTGAAAGGTAATACAG 13200

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Qy 1561 cacattccaaattttaaataaaaagcatttactcaattattataaaacaacatatttataaa 1620
13561 CACATTCCAAATTTTAAATAAAAAGCATTTACTCAATTATTATAAAACAACATATTATAAA 13620

Qy 1621 agatgaaccacacacaaaggtcatcaaaacacactttttataaattagataaattctacctgt 1680
Db 13621 AGATGAACCACAC'AAAGGTCATCAAAACACCTTTTATAAATTAGATAATTCTACCTGT 13680



information about the form and the sequencing at <http://www.cis.upenn.edu/~davis>.

FEATURES
SOURCE

Source

Location/Qualifiers
1. .745

FORGIVENESS IS A SUFFICIENT

Job Analysis

Chrysomelidae

Column: "KELT-5b" 14.24

colours in the foreground but of

[illegible]

1. *Chlorophyll a* (Chl *a*)

[illegible]

715511 • *See* 715510

712.

7.3.3

14.

Library Match

Henry Macell




```

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Prod. No. is the number of reads predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	687.2	40.9	799	112	HEM004502	A1340926 Homo sapi
2	610	36.3	541	135	HEM004502	HEM004502 Homo sapi
3	545.4	32.5	579	3	AA193409	AA193409 Zm m008.1
4	537.2	32.5	594	27	AA193409	AA193409 Zm m008.1
5	526.2	31.3	545	111	HEM004502	HEM004502 Homo sapi
6	523.8	31.2	541	8	AA527684	AA527684 HBB6406.8
7	519.2	30.9	573	8	AA528241	AA528241 HBB6406.8
8	518.6	29.9	556	92	AA528241	AA528241 HBB6406.8
9	509.4	30.3	511	20	AA461691	AA461691 HBB6406.8
10	490	29.2	509	87	AA235706	AA235706 HBB6406.8
11	383.1	28.5	493	39	AA528241	AA528241 HBB6406.8
12	381.8	28.7	496	4	AA528241	AA528241 HBB6406.8
13	375.4	28.3	477	16	AA1090024	AA1090024 HBB6406.8
14	367.6	27.8	786	17	AA1174913	AA1174913 HBB6406.8
15	364	27.6	464	7	AA426446	AA426446 Zm m008.1
16	364	27.6	464	24	AA1712337	AA1712337 Zm m008.1
17	363.6	27.5	479	23	AA1090024	AA1090024 HBB6406.8
18	362.4	27.5	476	15	AA1090024	AA1090024 HBB6406.8
19	362.4	27.5	485	13	AA528241	AA528241 HBB6406.8
20	359.6	27.4	477	88	AA528241	AA528241 HBB6406.8
21	359	27.3	594	7	AA528241	AA528241 HBB6406.8
22	353.4	27.0	462	1	AA040801	AA040801 HBB6406.8
23	353	27.0	478	1	AA040801	AA040801 HBB6406.8
24	353	27.0	503	1	AA041239	AA041239 HBB6406.8
25	349	26.7	469	15	AA1056055	AA1056055 HBB6406.8
26	348.1	26.7	450	138	AA1056055	AA1056055 HBB6406.8
27	344.6	26.5	462	20	AA1118295	AA1118295 HBB6406.8
28	343.4	26.4	466	25	AA1090024	AA1090024 HBB6406.8
29	343.4	26.3	466	25	AA1090024	AA1090024 HBB6406.8
30	343.4	26.0	467	22	AA1090024	AA1090024 HBB6406.8
31	342.9	25.6	742	157	AA1090024	AA1090024 HBB6406.8
32	342.9	25.6	441	10	AA683232	AA683232 HBB6406.8
33	342.9	25.4	455	4	AA683232	AA683232 HBB6406.8
34	342.9	25.3	460	40	AA1090024	AA1090024 HBB6406.8
35	342.4	25.3	427	11	AA706441	AA706441 HBB6406.8
36	342.4	25.2	444	15	AA1056055	AA1056055 HBB6406.8
37	342.4	25.2	449	19	AA1056055	AA1056055 HBB6406.8
38	342.4	25.1	427	25	AA1090024	AA1090024 HBB6406.8
39	341.6	24.8	424	25	AA1090024	AA1090024 HBB6406.8
40	341.6	24.7	443	16	AA110924	AA110924 HBB6406.8
41	340.4	24.2	420	3	AA1090024	AA1090024 HBB6406.8
42	339	24.2	417	7	AA1090024	AA1090024 HBB6406.8
43	305.6	24.1	431	13	AA1090024	AA1090024 HBB6406.8
44	305.2	24.1	426	96	AA1090024	AA1090024 HBB6406.8
45	306	23.6	480	18	AA1090024	AA1090024 HBB6406.8

ALIGNMENTS

RESULT 1
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 ID HEM004502 Standard: RNA, EST: 769 bp.
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 AC A1040026
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 DI 12 MAR 1999 (rel. 59, created)

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3	22	44.5	2.7	164.79	5.4	FEAR1-396	Z98551	Plasmodium
3	23	45	2.7	110.59	5.4	FEAR1	111172	Plasmodium
3	24	45	2.7	146.85	5.4	AT005084	AC005084	Homo sapi
3	25	44.8	2.7	135.54	7	ATFA001408	AT001408	Arabidops
3	26	44.8	2.7	198.20	7	ATCHR1V5	AT16149	Arabidops
3	27	44.8	2.7	21.447	70	AT454795	AT454795	Homo sapi
3	28	44.6	2.7	98.53	64	U32818	U32818	Homo sapi
3	29	44.6	2.7	46.274	5.4	AC011680	AC011680	Homo sapi
3	30	44.6	2.7	110.76	5.4	FEAR1-313	Z98547	Plasmodium
3	31	44.4	2.6	2.12	5.4	MEM118A	124561	MC0154372
3	32	44.4	2.6	18.618	49	AC025896	AC025896	Homo sapi
3	33	44.4	2.6	215.46	56	AT074613	AT074613	Homo sapi
3	34	44	2.6	746.2	7	CPLA1	X52578	MC0139191
3	35	44	2.6	116.85	5.2	HES13C22	X51021	Homo sapi
3	36	43.8	2.6	61.306	9	AC007474.3	AC007474.3	Homo sapi
3	37	43.8	2.6	479.92	5.4	FEAR1-133	AC037125	Plasma
3	38	43.8	2.6	151.909	9	AC025248	AC025248	Homo sapi
3	39	43.8	2.6	16.593	7.5	AT051567	AT051567	Homo sapi
3	40	43.8	2.6	19.9551	26	AT0064281	AT0064281	Homo sapi
3	41	43.6	2.6	2.840	29	AT422936	AT122936	Homo sapi
3	42	43.6	2.6	175.97	6.9	HS18141.10	AT122978	Homo sapi
3	43	43.6	2.6	84.711	7	AT0029047	AT0029047	Homo sapi
3	44	43.6	2.6	114.940	6	AT0069922	AT0069922	Arabidops
3	45	43.6	2.6	159.68	6.4	AT157761	AT157761	Homo sapi

ALUMINUM

TITLE
JOURNAL
REFERENCE
AUTHORS

Nath, R., Naylor, J., Nilom, M., O'Donnell, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Stange-Thumann, N., Stillwell, L., Stojanovic, N., Stone, C., Subramanian, A., Testage, S., Thibault, R., Tortorella-Miller, I., Vassiliou, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W., Zeng, X., and Zeng, M.

Direct Submission
Submitted (28 Aug-1990) Microfilm Institute/MPI Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 118276)

Britten, D., Fisman, K., Hinton, L., Nishbaum, C., Landry, E., Allen, N., Miller, P., Robert, J., Baldwin, J., Burton, N., Boocky, R., Bennett, S., Brown, A., Castle, A., Gentry, G., Goldstein, M., Hollingsworth, S., Kellymo, C., Clarke, T., Collins, D., Depierre, F., Evans, K., Owen, K., Demeland, J., Fortin, P., FitzHugh, W., Frost, C., Fuller, R., Garay, S., Gaudin, S., Gray, C., Grand, S., Hughes, B., Heutloff, A., Herma, L., Horton, L., Howland, J.C., Jacobson, J., Jones, C., Kammer, K., Kasas, A., Lechewsky, J., Macdonald, P., Margulis, R., McKean, P., Mitchell, A., Myerberg, K., Mulholland, B., Mullis, M., Nelson, W., Olden, M., Orskov, J., Reid, R., Rayford, J., Ribicki, M., Robinson, T., O'Donnell, P., Taylor, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Stange-Thumann, N., Stillwell, L., Stojanovic, N., Stone, C., Subramanian, A., Testage, S., Thibault, R., Tortorella-Miller, I.,

[illegible]

TITLE	FEATURES
<p>Journal Submission</p> <p>Submitted (06/JUN/2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA</p> <p>On Aug 28, 1998 this sequence version replaced g14492743.</p> <p>All repeats were identified using RepeatMasker (Smith, A.F.A. & Green, P. (1996 1997)</p> <p>g14492743: gene = "wdr5", n = 30, map_pos = 4, Master.html location/Qualifiers</p> <p>1..118276</p>	<p>source</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/chromosome="17"</p> <p>/map_pos="17"</p> <p>/clone="HCl152475"</p> <p>/clone_lib="c111c human BAC"</p> <p>/complement(2575..592)</p> <p>/rpt_family "AlusA"</p> <p>/complement(1063..11704)</p> <p>/rpt_family "11M8"</p> <p>1279..1276</p> <p>/rpt_family "CA)n"</p> <p>/complement(1279..1468)</p> <p>/rpt_family "11M8"</p> <p>/complement(1412..1452)</p> <p>/rpt_family "Alu153"</p> <p>/complement(1975..2142)</p> <p>/rpt_family "Alu153"</p> <p>/complement(2143..2155)</p> <p>/rpt_family "AlusA"</p> <p>/complement(2116..2194)</p> <p>/rpt_family "TTAAAn"</p> <p>/complement(2115..2480)</p> <p>/rpt_family "AlusA"</p> <p>/complement(2481..2415)</p> <p>/rpt_family "Al153"</p> <p>/complement(2635..2662)</p> <p>/rpt_family "PolyA"</p> <p>2949..3260</p> <p>/rpt_family "Alu1b"</p> <p>/complement(3391..3401)</p> <p>/rpt_family "AlusA"</p> <p>/complement(3462..3428)</p> <p>/rpt_family "TTAAAn"</p> <p>/complement(3429..3677)</p> <p>/rpt_family "AlusA"</p> <p>3734..3884</p> <p>/rpt_family "TBM"</p>

RESULT 4
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AC015727.175639 bp DNA HUG 09-SEP-2000
SEQUENCE. 41 unordered pieces.
AC015727
AC015727.4 6110045179
HUG HUGS_HUGS11: HUGS_HUGS11
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo.
1 (bases 1 to 175649)
Britten, D., Linton, L., Musburger, C., and Lander, E.
Homo sapiens chromosome 17, clone RP11.420A6
Unpublished
2 (bases 1 to 175649)
Britten, D., Linton, L., Musburger, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, I., Barina, N., Beckwith, R., Bergelson, L., Bonkshaiter, B.,
Brock, A., Castle, A., Collamore, M., Collins, S., Collamore, A.,
Cook, T., D'Arcangelo, K., Deary, K., Fleming, M., Dencher, L., Doyle, M.,
Fertig, J., Fitzhugh, W., Forrest, C., Fink, K., Galt, B.,
Gallagher, J., Gargyula, S., Grant, G., Hayes, R., Heath, A., Horton, L.,
Howard, J., Johnson, E., Jones, K., Kama, L., Kataras, A., Kibbi, J.,
Leibovitz, J., Li, G., Locke, K., Macpherson, J., Marquis, N.,
McKenna, J., McGrath, A., Mennard, K., Mervin, J., Middleton, J.,
Mortimer, J., Naylor, J., Norman, H., O'Connor, J., O'Donnell, J.,
Patterson, K., Pfaller, V., Pflanz, P., Ray, A., Santos, K., Seery, P.,
Stadler, J., Stojanovic, N., Subramanian, A., Talamas, J.,
Tetlow, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, J., Ye, M., Zimmer, A., and Zody, M.
Direct Submission
Submitted (17 MAY 1999) Whole-genome shotgun project for genome
research, 420 Charles Street, Cambridge, MA 02141, USA
on Sep. 9, 2000 this sequence version replaced at 16964075.
All repeats were identified using RepeatMasker.
Smith, A.F.A. & Green, P. (1996) 1997
http://www.genome.washington.edu/gen/human.chrom1
Genome Center
Center: Whitehead Institute of MIT Center for Genome Research
Center code: WIMR
Web site: <http://www.scrip.mit.edu>
Contact: submissions@genome.wi.mit.edu
Project Information
Project name: 420 A6
Project clone name: 420 A6
Summary statistics
Sequencing vector: M13, 877815, 878 of reads
Sequencing vector: Plasmid, 176, 138 of reads
Chemistry: Dye primer, amersham, 48 of reads
Chemistry: Dye-terminator B14 dye, 968 of reads
Assembly program: Phrap, version 0.960741
Consensus quality: 161512 bases at least Q40
Consensus quality: 167866 bases at least Q30
Consensus quality: 170654 bases at least Q20
Insert size: 170000; average: 117
Insert size: 172639; sum of overlaps
Quality: average: 4.7; min: 2.0; max: 5.0
NOTE: This is a working draft sequence. It currently
consists of 41 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1 13947: contig of 13947 bp in length
* 1048 14047: gap of 100 bp
* 14048 14259: contig of 212 bp in length
* 14260 14359: gap of 100 bp
* 14360 15140: contig of 680 bp in length

15040 15139: gap of 100 bp
* 15140 15832: contig of 693 bp in length
* 15833 15932: gap of 100 bp
* 15933 16689: contig of 757 bp in length
* 16690 16789: gap of 100 bp
* 16790 18092: contig of 1303 bp in length
* 18093 18192: gap of 100 bp
* 18193 19993: contig of 1801 bp in length
* 19994 20093: gap of 100 bp
* 20094 22205: contig of 2112 bp in length
* 22206 22305: gap of 100 bp
* 22306 23915: contig of 1610 bp in length
* 23916 24015: gap of 100 bp
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* 26545 26644: gap of 100 bp
* 26645 28851: contig of 2207 bp in length
* 28852 28951: gap of 100 bp
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* 30455 30554: gap of 100 bp
* 30555 32015: contig of 2461 bp in length
* 32016 33727: contig of 2612 bp in length
* 33728 35827: gap of 100 bp
* 35828 59251: contig of 23428 bp in length
* 59256 59355: gap of 100 bp
* 59356 62539: contig of 3184 bp in length
* 62540 62639: gap of 100 bp
* 62640 62730: contig of 5991 bp in length
* 62731 68030: gap of 100 bp
* 68031 73174: contig of 5144 bp in length
* 73175 73274: gap of 100 bp
* 73275 77427: contig of 4153 bp in length
* 77428 77527: gap of 100 bp
* 77528 81788: contig of 4261 bp in length
* 81789 81988: gap of 100 bp
* 81889 86379: contig of 4491 bp in length
* 86380 86479: gap of 100 bp
* 86480 91547: contig of 5068 bp in length
* 91548 91647: gap of 100 bp
* 91648 92783: contig of 5136 bp in length
* 92784 97883: gap of 100 bp
* 97884 105190: contig of 7307 bp in length
* 105191 105290: gap of 100 bp
* 105291 111855: contig of 6565 bp in length
* 111856 111955: gap of 100 bp
* 111956 119820: contig of 7865 bp in length
* 119821 119920: gap of 100 bp
* 119921 141299: contig of 11479 bp in length
* 141300 141399: gap of 100 bp
* 141400 139546: contig of 8147 bp in length
* 139547 139646: gap of 100 bp
* 139647 155538: contig of 15892 bp in length
* 155539 155638: gap of 100 bp
* 155639 173481: contig of 17843 bp in length
* 173482 173581: gap of 100 bp
* 173582 175639: contig of 2058 bp in length.
1. 175639
Location/Qualifiers
/feature="Name: sapiens"
/feature="contig:9606"
/feature="17"
/map="17"
/feature="RP11 420A6"
/feature="11b-RP11 Human Male YAC"
1. 13947
/feature="assembly: fragment"
/feature="end:SP6"
/feature="side:1011"
/feature="14259"
/feature="assembly: fragment"
/feature="15049"
/feature="assembly: fragment"
15140. 15832

NAME: Kozlov, S., Hudson, J., Lipshutz, R., Chee, M., and
Lander, E.S.
Large-scale identification, mapping, and genotyping of
single nucleotide polymorphisms in the human genome
Science 268 (5144): 1072-1078 (1998)

COMMENT

SYNOPSIS: STS EST65781
Contact: Thomas Hudson
Whitehead Institute, MIT, Center for Genome Research,
Whitehead Institute for Biomedical Research,
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu
Primer A: GGTATGACCTTTTAAATTT
Primer B: TGTCAGACATGATGATGAC
STS size: 142
PCR product:

Protocol:
Incubation: 94 degrees C for 4.00 minutes
Annealing: 94 degrees C for 50.0 seconds
Polymerization: 58 degrees C for 1.50 minutes
PCR cycles: 72 degrees C for 1.00 minutes
Thermal cycler: custom built by IAS, Costar, Cambridge MA

Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: 4 mM
Total Polymerase: 0.5 U
Total Vol: 20 ul

Butter:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
Gelatin: 0.01 %
Location/Qualifiers

FEATURES
SOURCE: 1, 142
Organization: "Homo sapiens"
chr12: chr12:142000000
Map: "7.60 cR from top of Chr17 linkage group"
Feature: "Human RefSeq"
Note: "STS derived from sequences in dbEST and the
Oncogene collection."

STS
Primer_bind
Primer_bind
BASE COUNT: 41 a 36 c 26 g 48 t 1 others
ORIGIN

Query Match: 8.48; Score 141; DB 75; Length 142;
Best Local Similarity: 99.38; Pred. No. 6e 20;
Matches 141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match: 8.48; Score 141; DB 75; Length 142;
Best Local Similarity: 99.38; Pred. No. 6e 20;
Matches 141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
659 407/7 142 bp DNA STS 30 MAR 2000
DEFINITION STS: 140001 Human homo sapiens STS genomic, sequence tagged site,
ACCESSION U59407

VECTER
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

659407.1 01:54:24626
human.
Homo sapiens
Eukaryote; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Olivieri, M., and Cox, D.R.
Exp. Med. and Biol. 40: 142 (2000)
Unpublished (2000)

Contact: Michael Olivieri, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave., 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivieri@shgc.stanford.edu
Primer A: TGAACATCTCTCTGACATCA
Primer B: GCTTTCACATCTCTGACATCT
STS size: 100
PCR product:

Protocol:
Incubation: 95 degrees C for 10 minutes
Annealing: 94 degrees C for 30 seconds
Polymerization: 72 degrees C for 24 seconds
PCR cycles: 40
Thermal cycler: Perkin Elmer 9700

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Ampliflag Gold Polymerase: 5 ul
Total Vol: 5 ul

Butter:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3
Location/Qualifiers

FEATURES
SOURCE: 1, 142
Organization: "Homo sapiens"
chr12: chr12:142000000
Map: "17"
Feature: "Human"
Note: "STS derived from sequences in dbEST and the
Oncogene collection."

STS
Primer_bind
Primer_bind
BASE COUNT: 41 a 36 c 26 g 48 t 1 others
ORIGIN

Query Match: 8.48; Score 141; DB 75; Length 142;
Best Local Similarity: 99.38; Pred. No. 6e 20;
Matches 141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match: 8.48; Score 141; DB 75; Length 142;
Best Local Similarity: 99.38; Pred. No. 6e 20;
Matches 141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

